

by the appropriate provision authorizing payment of the required fee; (17) a revised PTO form 1449; and (18) copies of references AA-DQ listed on the revised PTO form 1449.

It is estimated that no additional fee is required for filing this Amendment. However, should the Patent Office determine otherwise, please charge the necessary fee to Pennie & Edmonds LLP Deposit Account No. 16-1150.

**IN THE SPECIFICATION:**

Please amend the specification as follows:

On page 1, please replace the paragraph beginning at line 3 with the following paragraph:

This application is a continuation-in-part of U.S. Application Serial No. 09/503,387, filed February 14, 2000, which is a continuation-in-part of U.S. Application Serial No. 09/454,824, filed December 6, 1999, which is a continuation-in-part of U.S. Application Serial No. 09/345,068, filed June 30, 1999, the entire contents of each of which is incorporated herein by reference its entirety.

On page 14, please replace the paragraph beginning at line 25 with the following paragraph:

FIGURES 3A-3C depict an alignment of the nucleotide sequence of the open reading frame for human monocyte inhibitory receptor precursor (SEQ ID NO:24; GenBank Accession Number U91928) and the nucleotide sequence of the open reading frame for human TANGO 268 (SEQ ID NO:2). The nucleotide sequences of coding regions of human monocyte inhibitory receptor precursor and human TANGO 268 are 37.7% identical. The nucleotide sequences of full-length, including the 5' and 3' untranslated regions (UTRs), human monocyte inhibitory receptor precursor SEQ ID NO:11; GenBank Accession Number U91928) and human TANGO 268 are 49.9% identical. These alignments were performed using the ALIGN alignment program with a PAM120 scoring matrix, a gap length penalty of 12, and a gap penalty of 4.

On page 14, please replace the paragraph beginning at line 35 with the following paragraph:

FIGURE 4 depicts an alignment of the amino acid sequence of human monocyte inhibitory receptor precursor (SEQ ID NO:12) and the amino acid sequence of human TANGO 268 (SEQ ID NO:3). The amino acid sequences of human monocyte inhibitory receptor precursor and human TANGO 268 are 23.0% identical. This alignment was performed using the ALIGN alignment program with a PAM120 scoring matrix, a gap length penalty of 12, and a gap penalty of 4.

On page 16, please replace the paragraph beginning at line 1 with the following paragraph:

FIGURE 9 depicts an alignment of the amino acid sequence of human monocyte inhibitory receptor precursor (SEQ ID NO:12) and the amino acid sequence of mouse TANGO 268 (SEQ ID NO:16). The amino acid sequences of human monocyte inhibitory receptor precursor and mouse TANGO 268 are 20.3% identical. This alignment was performed using the ALIGN alignment program with a PAM120 scoring matrix, a gap length penalty of 12, and a gap penalty of 4.

On page 19, please replace the paragraph beginning at line 24 with the following paragraph:

FIGURES 25A-25I: FACS analysis of the seven unique scFv's. Purified scFv's were incubated with U937 cells expressing GPVI (GPVI-U937 cells) and the binding of scFv's to GPVI-U937 cells was detected by FACS analysis.

On page 27, please replace the paragraph beginning at line 10 with the following paragraph:

Figure 3A-3C show an alignment of the human TANGO 268 coding region (SEQ ID NO:2) with the human monocyte inhibitory receptor precursor protein coding region (SEQ ID NO:24). The human monocyte inhibitory receptor has been shown to downregulate activation responses by phosphatases. The nucleotide sequences of coding regions of human monocyte inhibitory receptor precursor and human TANGO 268 are 37.7% identical. The full-length nucleic acid sequence of human TANGO 268 (SEQ ID NO:1) exhibits 49.9% identity to the full-length nucleic acid human monocyte inhibitory receptor precursor (SEQ ID NO:11; Accession Number U91928).

On page 27, please replace the paragraph beginning at line 18 with the following paragraph:

Figure 4 shows that there is an overall 23% identity between the amino acid sequence of the human TANGO 268 protein and the amino acid sequence of the human monocyte inhibitory receptor protein (SEQ ID NO:12; Accession Number U91928).

On page 30, please replace the paragraph beginning at line 9 with the following paragraph:

In general, mouse TANGO 268 has most homology to various members of the immunoglobulin superfamily that includes NK inhibitory and activating receptors and Fc receptors. The full-length nucleic acid sequence of mouse TANGO 268 exhibits 35.6% identity to the full-length nucleic acid human monocyte inhibitory receptor precursor (SEQ ID NO:11; Accession Number U91928). Figures 8A-8B show an alignment of the mouse TANGO 268 coding region (SEQ ID NO:15) with the human monocyte inhibitory receptor precursor protein coding region (SEQ ID NO:24). The nucleotide sequences of the coding regions of human monocyte inhibitory receptor precursor and mouse TANGO 268 are 34.4% identical. The nucleotide sequences of the full-length human monocyte inhibitory receptor precursor (SEQ ID NO:11; Accession Number U91928) and full-length mouse TANGO 268 (SEQ ID NO:14) are 35.6% identical. Figure 9 shows that there is an overall 20.3% identity between the mouse TANGO 268 amino acid sequence and the human monocyte inhibitory receptor protein amino acid sequence (SEQ ID NO:12; Accession Number U91928).

On page 54, please replace the paragraph beginning at line 31 with the following paragraph:

Microtiter plates (ImmulonII Dynex) were coated with type I or type III collagen (40 µg/mL in 20 mM CH<sub>3</sub>COOH) overnight at 4°C and then saturated with 2 mg/mL BSA for two hours at room temperature. Soluble human GPVI-Fc (5 nM in PBS pH 7.4 containing 0.2% BSA and 0.1 % Tween) in the absence or the presence of antibodies (10 µg/mL) was added to the wells of the microtiter plate and the plates were incubated for two hours at room temperature. After washing the wells, peroxidase coupled protein A (Amersham) was added to the wells and the plates were incubated for 2 hours at room temperature. After washing, peroxidase substrate was added and OD was measured at 495 nm.

On page 55, please replace the paragraph beginning at line 3 with the following paragraph:

Microtiter plates (ImmulonII Dynex) were coated with monoclonal antibody 1P10.2 (5 µg/mL in PBS) overnight at 4°C and then saturated with 2 mg/mL BSA two hours at room temperature. Soluble human GPVI-Fc (0.5 nM in PBS pH 7.4 containing 0.2% BSA and 0.1 % tween) was added to the wells of the plate and the plate was incubated for two hours at room temperature. After washing the wells, buffer or antibodies (10 µg/mL) were added to the wells and the plates were incubated for one hour at room temperature. Next, <sup>125</sup>I-labeled convulxin (~1 nM) was added to the wells and the plates were incubated for approximately 10 minutes. The wells were washed and counted for <sup>125</sup>I-convulxin binding in a gamma counter.

On page 56, please replace the paragraph beginning at line 1 with the following paragraph:

Bst NI fingerprinting of the 28 positive clones is shown in Figure 24. A total of seven unique clones were found of the pool. All of seven of the clones recognized GPVI on transduced cells in a FACS experiment (Figures 25A-25I). CDR sequences of scFvs are shown in Table 7 below.

#### **IN THE CLAIMS:**

Please amend the claims, as follows:

Cancel claims 137, 139, 141, 143, 145, 147, 149, 151, 153, 156, 158, 160, 166, 167, 170, 172, 174, 179, 182, 184, 186, 190, 193, 195, 197, 202, 204, 206, 209, 214, 217, 219, 221, 225, 228, 230, 232, 236, 239, 241, 243, 244, 253 and 255, without prejudice.

Amend claims 132, 140, 144, 148, 152, 159, 245-247, 254, and 256-264 to read as follows:

132. (Amended) A substantially purified antibody comprising a complementarity determining region (CDR) having an amino acid sequence of a CDR encoded by the cDNA insert of the plasmid deposited with the ATCC® as patent deposit Number PTA-2442, wherein said antibody immunospecifically binds to a human TANGO 268 antigen.